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Minimum DB seq length: 0
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Gapop 10.0 , Gapext 0.5
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1198
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                                                                                                                                                                                                                                                                                                                                                    2443163 seqs, 439378781 residues
                                                                                                                                                          A_Geneseq_21:*
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Listing first 45 s
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Copyright (c) 1993 - 2005 Compugen Ltd.
                  geneseqn1990s:*
geneseqn2000s:*
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geneseqn2003as:*
geneseqn2003bs:*
geneseqn2003bs:*
geneseqp2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	% Query Match Length	BB	ij	Description
1	1198	100.0	229	4	0	Human
N	1198	100.0	229	v	ABG34856	Human
ω	1198	•	231	4	AAM42009	Aam42009 Human pol
4	œ	11.6	164	ហ	ABG34855	Abg34855 Human cDN
υ	113		233	4.	AAM93668	Aam93668 Human pol
6	113	9.4	233	4	AAG93290	Aag93290 Human pro
7	113	9.4	233	7	ADJ69163	Human
8	113	9.4	233	œ	ADL31517	Adl31517 Human pro
9	92	7.7	695	ហ	ABB54167	Lacto
10	92	7.7	695	8	ADS29356	Bacte
11	90	7.5	269	4	AAC08972	Human
12	89	7.4	572	8	ABM83354	Abm83354 Human dia
13	89	7.4	623	4.	AAB93182	Human
14	89	7.4	623	υ	ABB97233	Novel
15	89	7.4	652	4.	AAB93168	
16	89	7.4	664	Δ.	AAB83843	Amino
17	89	7.4	664	4	AAB20219	Aab20219 Human Chf
18	88.5	7.4	388	8	ADQ08702	Adq08702 Ciona int
19	87.5	7.3	1245	7	ADC32818	Human
20	86.5	7.2	470	œ	ABM83305	
21	86.5	7.2	669	σ	ABU23878	Abu23878 Protein e
22	86	7.2	158	7	ADH88711	Adh88711 Enterococ
23	85.5	7.1	571	8	ADU07910	Adu07910 Amino aci
24	84.5	7.1	485	ហ	ABP51336	Abp51336 Human MDD

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45	44	43	42	41	40	39	38	37	36	3 5	3.4 4.	ω ω	32	31	30	29	28	27	26	25
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6.9	6.9	6.9	6.9	6.9		6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.0
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AEA16977	ADN72405	AAY90242	ADX72944	ABU23749	AAW59465	AAW59456	AAP90110	AAW59496	AAW59464	AAW59460	AAW59462	AAW59459	AAW59458	AAW59457	AAW59463	AAW59461	ABM36197	AAU39678	ADC31196	AAB95788
Aea16977	Adn72405	Aay90242	Adx72944	Abu23749	Aaw59465	Aaw59456	Aap90110	Aaw59496	Aaw59464	Aaw59460	Aaw59462	Aaw59459	Aaw59458	Aaw59457	Aaw59463	Aaw59461	Abm36197	Aau39678	Adc31196	Aaby5/88
Arabidops	Thale	Human	Plant	Protein e	Microbial					Microbia	Microbia			Microbial	Microbia.	Microbia	gruordord	Propionia	Human	Human pro

ALIGNMENTS

RESULT 1 AAM40223 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; platheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; AAM40223 standard; protein; 229 AA. WO200153312-A1 Human polypeptide SEQ ID NO 3368. 22-OCT-2001 AAM40223; 26-DEC-2000; 2000WO-US034263 26-JUL-2001. Homo sapiens. leukaemia. (first entry)

23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-20000; 2000US-00662191.
19-CCT-2000; 2000US-00663036.
29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

Tang YT, Wang J, Zhou P, WPI; 2001-442253/47. N-PSDB; AAI59379. Liu C, Asundi V, Wang Z, Wehrman T, Goodrich R, Drmana Drmanac Chen R, Xu C, IC RT; Xue Ma a Ą, Qian XB, Yang Y, Ren F, Zhang c ч Wang D;

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Example 5; SEQ ID NO 3368; 10078pp; English.

or ribozyme of 85P1B3

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RESULT 2
ABG34856
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 229 AA;
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                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytostatic; 85P1B3; cancer; immunogen; chromosome 15q14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer related protein encoded by cDNA 85P1B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2002
Composition for modulating the status of 85P1B3 protein or a molecule comprising a substance e.g. antibody specific to, nucleic acid encoding,
                                                                                                                                                                                                                                                                       28-AUG-2000; 2000US-0228432P
                                                                                                                                                                                                                                                                                                                  28-AUG-2001; 2001WO-US026838
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200218578-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG34856 standard; protein; 229
                                                                         N-PSDB; ABK70506
                                                                                             WPI; 2002-382963/41.
                                                                                                                                                                       Raitano AB,
                                                                                                                                                                                                                         (AGEN-) AGENSYS INC.
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Pred. No. 9.7e-127;
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\mathbb{P}_{\mathbf{x}}^{\mathsf{x}} \mathbb{P}_{\mathbf{x}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC position having a value greater than 0.5 in the beta-turn profile; a cc polynucleotide that encodes analogue peptide of 8, 9, 10 or 11 contiguous CC residues of the 85P1B3 protein; a recombinant protein comprising the CC antigen-binding region of a monoclonal antibody; a non-human transgenic animal that produces an antibody specific to the 95P1B3 protein; a single chain CC monoclonal antibody (MAD) that comprises the variable domains of the CC enter cells or treating a patient who bears cancer cells that expresses the protein; a vector CC comprising the protein, by administering the protein antibody, polynucleotide, CC ribozyme that cleaves the polynucleotide and T cells that expresses the protein antibody specific to the mammal's immune response CC directed to the protein; and generating a mammalian immune response CC divering a cytotoxic agent to a cell that expresses the protein exposing cells of the mammal's immune system to the antibody-agent conjugate to the protein, is useful for the antibody-agent conjugated to antibods are useful for in the antibody-agent conjugated to antibods are useful for inhibiting growth of cancer cells or reating a mammalian immune response CC directed to the protein, for detecting a mammalian immune response the protein or generating a mammalian immune response to the antibody-agent conjugated to antibody and exposing the cell conjugated to antibody and exposing the cell conjugated to antibody and exposing the cell capted to the protein, for detecting a mammalian immune response conserved in the protein or polynucleotide in a biological sample in a biological sample from a patient who has or who is suspected of having cancer. The generating a mammalian immune response to the grotein or spilas is located on human chromosome 15q14. The present
                                                                                                                                                           Query Match
Best Local S
Matches 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is the 85P1B3 protein
                                                                                                                                                           Local Sim thes 229;
1 MAAQPIRHRSRCATPPRGDFCGGTERAIDQÅSFTTSMEWDTQVVKGSSPLGPAGLGAEEP
                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             229
                                                                                                                                                                  100.0%; Score 119%; DB 5; llarity 100.0%; Pred. No. 9.7e-127; Conservative 0; Mismatches 0;
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RESULT 3
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                                                      standard; protein; 231
                                                                                                                                 NASEMDIONVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDOSKPEN 229
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(first entry)
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MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP

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cytostatic; gene therapy; cancer; y; central nervous system; CNS;

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Matches 229
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25-APR-2000; 2000US-00553317.

20-JUN-2000; 2000US-00598042:

19-JUL-2000; 2000US-00620312.

03-AUG-2000; 2000US-00623450.

14-SEP-2000; 2000US-00663191.

19-OCT-2000; 2000US-00693036.

29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                        immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Augotrophic lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; halzheimer's; Parkinson's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                 Sequence 231 AA;
                                                                                                                                                                                                                                                                part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1
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                                                                                                                                                                                 ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-442253/47.
   121.VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
                                                                                                                                                                 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide SEQ ID NO
                                  63
                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; immunosuppressant;
                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
Wang Z,
Goodrich
                                                                                                                    MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
                                                AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL 120
                                                                                                MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
                                  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6940; 10078pp; English.
                                                                                                                                                                                                                                                                printed specification
                                                                                                                                                                 Conservative
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R, Drma
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Wehrman T,
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Score 1198; DB 4; Pred. No. 9.8e-127; ; Mismatches 0;

Length Indels

<u>,,</u>

Gaps

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Drmanac

Chen R, Xu C, IC RT;

Xue Ma Α, Y,

Qian XB, Yang Y,

Ren F, Zhang ,

Ç Wang D;

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ARBSULT 4
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ARBG1487
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                                                                                                                                                                                                                                                                     CC emprising a peptide region of 5 amino_acids of the 85P1B3 gene product is modulated. Also included are a composition CC comprising a peptide region of 5 amino_acids of the 85P1B3 protein, in CC any whole number increment up to 229 that includes an as position CC selected from an as position having a value greater than 0.5 in the CC Hydrophilicity profile, an as position having a value less than 0.5 in the hydropathicity profile, an as position having a value greater than 0.5 in the percent accessible residue profile, an as position having a value greater than 0.5 in the average flexibility profile, or an as CC value greater than 0.5 in the average flexibility profile, or an as CC polynucleotide that encodes analogue peptide of 8, 9, 10 or 11 contiguous cresidues of the 85P1B3 protein; a recombinant protein comprising the CC antigen-binding region of a monoclonal antibody; a non-human transgenic CC animal that produces an antibody specific to the protein; a single chain CC monoclonal antibody (MAb) that comprises the variable domains of the heavy and monoclonal antibodies specific to the protein; a vector CC comprising a polynucleotide that encodes the MAb; inhibiting growth of cancer cells or treating a patient who bears cancer cells that expresses the protein, by administering the protein, antibody, polynucleotide.
encoding the protein, antisense polynucleotide to the polynucleotide, ribozyme that cleaves the polynucleotide and T cells that specifically recognize the protein; and generating a mammalian immune response directed to the protein exposing cells of the mammal's immune system to an immunogenic portion of the protein or polynucleotide. The composition, which comprises an antibody specific to the protein, is useful for delivering a cytotoxic agent to a cell that expresses the protein by providing a cytotoxic agent conjugated to antibody and exposing the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for modulating the status comprising a substance e.g. antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or ribozyme of 85P1B3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytostatic; 85P1B3; cancer; immunogen; chromosome 15q14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA 85P1B3 splice variant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising a substance that modulate the status of 85P1B3, where the status of a cell expresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 38; Page 124; 201pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hubert RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the status of 85P1B3 protein or a molecule antibody specific to, nucleic acid encoding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      open reading
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the antibody-agent conjugate. The methods are useful for inhibiting growth of cancer cells or treating a patient who bears cancer cells that expresses the protein, for generating a mammalian immune response directed to the protein, for detecting the presence of the protein or polynucleotide in a biological sample in a patient who has or who is suspected of having cancer and for monitoring 85P1B3 in a biological sample from a patient who has or who is suspected of having cancer. The gene for 85P1B3 is located on human chromosome 15q14. The present
                                        clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cannot any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide,
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                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                 Ota T,
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                                                                                                                                                                                                                           Claim 8; SEQ ID NO 3550; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                  Wakamatsu
                                                                                                                                                                                            The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                            (HELI-)
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                                                                                                                                                                                                                                                       O Primers useful for synthesizing genetic manipulation.
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                               directly from EPO
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2000JP-00118774.
2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                                             cawa T, Isogai
Sugiyama T, Na
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:
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82.1%;
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1; Mismatches
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K, Kojima
                                                                                                                                                                                                                                                                       full length cDNA clones
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.8.6e-07;
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S, Otsuki
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                  Koga
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Best Local Similarity
Matches 52; Conserv
                                                    The present sequence is a human protein. The human protein, preferable originated from tumour cell line, is applicable as a drug, a reagent studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding sequence is useful for gene diagnosis and gene therapy expression vectors and transformant cells for detection of ligands as
                                                                                                                                                                                                                                                                                                                 Human protein originated from tumor cell line, applicable as reagent for studying intracellular protein networks and prote for drug screening, also encoded cDNA for gene diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein HP10650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato
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30-MAY-2000;
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10-FEB-2000;
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06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAH68575
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; 2000JP-00034090.
; 2000JP-00034091.
; 2000JP-00035829.
; 2000JP-00035899.
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2000JP-00160851.
                                                                                                                                                                                                                                      303-304; 471pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saeki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219
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Pred. No. 0.0011;
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                                                         agnosis and gene therapy detection of ligands and
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                              Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlative detecting a modified polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2002; 2002US-0372843P
17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2003; 2003WO-US010870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ69163 standard; protein;
                                                                                                                                                                       Claim 1; SEQ ID NO 969; 180pp; English
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Pred. No. 0.
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RESULT 8
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                                                                                                                                                           08-JUL-1999; 99JF-00118774.
11-JAN-2000; 2000JF-00118774.
02-MAY-2000; 2000JF-00183865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes a method fdr identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHOM), mitochondrial encephalopathy lattic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 233
                                                                                                                      Ota T,
                                                                                                                                                                                                                                    07-JUL-2000; 2003EP-00025638
                                                                                                                                                                                                                                                                                   EP1396543-A2
                                                                                                                                                                                                                                                                                                                                oligo-capping
                                                                                                                                                                                                                                                                                                                                                human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                       Human protein encoded by a full length cDNA clone SeqID 3550
                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                        ADL31517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL31517 standard;
                                                                                     WPI; 2004-204755/20
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                              New oligonucleotide primers
                                                                                                          Wakamatsu A,
                                                                                                                                                                                                                                                            10-MAR-2004.
                                                                                                                                                (REAS-)
                                 ength
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                  human cDNAs.
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Similarity 27.1%;
                                                                                                                       Nishikawa T,
                                                                        ADL31516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVLKALQMKLWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGYVYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASMWSSMSEDASV----ADMERAQL--EEEAAAAE-----ERPLVFLCSGCRRPLGDS
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                                                                                                          Sugiyama
                                                                                                                                                                                                                                                                                                                                      method
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                                                                                                          Isogai T,
a T, Nagai
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                                                (830
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                                                                                                            Hayashi K,
K, Kojima
                                                cDNAs)
                                                useful
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                                                                                                                          Ishii S,
                                                  for
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                                                                                                             Otsuki
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                                                synthesizing
                                                                                                             Kawai Y;
T, Koga
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Example 1; SEQ ID NO

3550; 1340pp; English

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RESULT 9
ABB54167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5° and 3° ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
                         acid
                                                                                       Claim
                                                                                                                 New nucleotide sequentiatis and related
                                                                                                                                                                                                                                                                                                                                                                 Biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2003
16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB54167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 233
                                                                                                                                                                                                                                    11-APR-2000;
                                                                                                                                                                                                                                                            11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                              FR2807446-A1
                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis;
                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB54167 standard; protein;
                                                                                                                                                                                                         (INRG ) INRA INST NAT
                                                                                                                                                                                                                                                                                    12-OCT-2001
                                                 sequence (ABA90521)
            species.
         present invention is related to a Lactococcus lactis nucleotide ence (ABA90521) and related proteins (ABB9300-ABB55621). The nuclei sequence is useful in the detection and/or amplification of nuclei sequence, particularly to identify Lactococcus lactis or related ies. The proteins of the invention are useful for the biosynthesis.
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                                                                                                                                                        2002-043418/06
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                                                                                         <u>د.</u>
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(first en
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                                                                                                                                                                                                                                                                                                                                                                 biodegradation;
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f
                                                                                                                             sequence useful in
                                                                                         NO 869; 2504pp;
                                                                                                                  species.
                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                  Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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Pred. No. 0.00:
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA
                                                                                                                                                                                                                                                                                                                                                                 lactic bacterium;
                                                                                         French.
                                                                                                                              the identification
                                                                                                                                                                                  Ehrlich
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                                                                                                                                                                                  SD
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                                                                                                                                 Lactococcus
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                                                   nucleic
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PD 18-1
XXX IS-
PD 20-1
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PD 21-
XXX (CAB
PDA (GC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen estimated modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                (CAOY/)
(HINK/)
(SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant cold tolerance; heat tolerance; drought tolerance; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial polypeptide #18389
                              The invention relates promoter functional in
                                                                                                     Claim
                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2003; 2003US-00369493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2004
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SLATER
CHEN X.
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                                                                                                                                                                                                                                                                                                                                                     GOLDMAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGTIIF-----FYSGTPFFSGAKGELKSRKPAMMLITMGITVAY-AYSVYATIMSLNG
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on relates to a recombinant DNA nctional in a plant cell, where expression of a polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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                                                                                                     18389; 122pp; English.
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                                                                                                                                                                                                                                                                                                     Slater
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92;
Pred. No.
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                                                                                                                                                                                                                                                                                                     Goldman
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     construct comprising a the promoter is positioned encoding a polypeptide from
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1 is available in
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; osmosis;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant.growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved plant.growth and development under at least one stress condition, improved lignin production or improved galactomannan condition. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant
                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 695 AA;
WPI; 2001-514838/56.
N-PSDB; AAI88903.
                                                                                                                                          28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                  07-SEP-2001.
                                                                                                                                                                                                                                                                                         WO200164835-A2
                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 22864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
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                                                                                                                                                                                                       26-FEB-2001; 2001WO-US004927.
                                                                                                 (HYSE-) HYSEQ INC.
                                                            ΥŢ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 IAELKEKIVLTHNRLKSLMKILSEVTPDQS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 LGTIIF-----FYSGTPFFSGAKGELKSRKPAMMMLITMGITVAY-AYSVYATIMSLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMGMNFWFELATLIVIMLIGHLIEMKAIMGAGDALKDLASLVPKKAHLKSGKDVELSELK
                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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25.3%;
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                                                            RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92; DB 8; Pred. No. 1.5;
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Best Local (
Mooney EM,
Stevens KA,
Peralta CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The
                                                                                                                                                                                                                                                                                                                                                 gene therapy; human diagnostic and therapeutic polynucleotide; dithp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004
                                                                        Schmidt JP,
                                                                                                                                               12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                   12-SEP-2003; 2003WO-US028227
                                                                                                                                                                                                                                           25-MAR-2004.
                                                                                                                                                                                                                                                                              WO2004023973-A2
                                                                                                                                                                                                                                                                                                                                                                                       Human diagnostic and therapeutic pprotein SEQ ID NO:3603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM83354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM83354 standard;
                                                       Harthshorne
                                                                                                             (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 LMALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ALAALRGHFCLS-----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 PMPDRRAEREQDPRVAPQ------QCAVC---LQPFCHLYWGCTRTGCYGCLA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ---GPAGLGAEEPAAGPOLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SLGAVVFSRVTNNVVLEAPFLVGIBGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
Delegeane AM, 1
Blanchard JL,
Anderson SB, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                      Wright RJ,
                                                       yht RJ, Bruns C
Suchorolski MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%; Score 90; DB 4; 23.0%; Pred. No. 0.58; ative 26; Mismatches 7
 Bruns CM, Marjanovic MM, Shen F;
ski MT, Altus CM, Pitts SJ, Elder I
Panesar IS, Banville SC, Reddy TP;
Panzer SR, Wang X, Au AP, Gersti
Rioux P, Shen EJ, Wu MC, Stuve LI
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                      Gerstin
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated used to diagnose a particular condition, disease or disorder associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
                                                                                                                                   Human; primer;
                                                                                                                                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                                           AAB93182 standard; protein; 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 572 AA;
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                                   07-FEB-2001
                                                                                                   Homo sapiens
28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMPDRRAEREQDPRVAPQ------QCAVC---LQPFCHLYWGCTRTGCYGCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                       sequence SEQ ID NO:12128.
                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitt UA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jackson JL,
                                                                                                                                                                                                                                                                                                                                                                 532
                                                                                                                                                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kirton ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gietzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                      486
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RESULT 14 ABB97233

ABB97233 standard; protein; 623

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ABB97233

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                                                                                                                                                                                                                                                                                                                                                                                                                        CC complementary strand of a polynucleotide which comprises on of the 5602 concelerate sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotide; or (b) a combination cof an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence complementary to a coligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence's end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in comparticularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC cANH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3563 represent coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, length cDNAs defined in the specification, and diagnosis of the abnormality of the proteins
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length cDNAs defined in the specification. Where a primer set compa
(a) an oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                         494
                                                                                                            100
                                                                                                                                                 450
                                                                                                                                                                                                                                                             8 HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL-----
                                                                                                                                                                                                                                                                                              Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 12128; 2537pp + Sequence Listing; English
                                  ALAALRGHFCLS-----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                 ----GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-----
                                                                                                                                                                                                                      YRRQAAQPPH---CPAPEGEPGAPQALGDAPPTSVSLTTAVQDYVCPLQGSHALCTCCFQ
LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYQQNIPASE
                                                                         PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNMI
                                                                                                          ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                                                                                                         623 AA;
                                                                                                                                                 PMPDRRAEREQDPRVAPQ------QCAVC---LQPFCHLYWGCTRTGCYGCLA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 99JP-00248036.
; 99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes primer sets
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                               7.4%;
                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                   Score 89; DB . Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cleotides, particularly the 5602 full-
cation, and for the detection and/or
proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                    DB 4; Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otsuki
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer set comprises:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                             TES
                                                                                                                                                                                                                            449
                                                                             537
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27-JUN-2002

(first

entry)

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RESULT 15
AAB93168
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BXXXB
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Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               (BSTs). They can be used to stimulate cell growth, to regulate e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-292408/33.
N-PSDB; ABN32419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human protein
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 501; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated polynucleotide for treating diseases associated encoded polypeptide such as cancer and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2000; 2000US-00659671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2001; 2001WO-US026015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200222660-A2
26-JUN-2001
                                                  AAB93168
                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                   393
                                                                                                                     538
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                                                                                                                                                                                                                                                        51
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                                                                                                                                                                                                                                                                                                                                     l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang Y,
                                                                                                                                                                                                                                                                                 YRRQAAQPPH---CPAPEGEPGAPQALGDAPPTSVSLTTAVQDYVCPLQGSHALCTCCFQ 449
                                                                                                                                                                                                                                                                                                            HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL-----
                                                  standard;
                                                                                                                                              ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE
                                                                                                                                                                                                                             PMPDRRAEREQDPRVAPQ------QCAVC---LQPFCHLYWGCTRTGCYGCLA 493
                                                                                                                                                                                                                                                                                                                                                                                            623 AA;
                                                                                                                   LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYQQNIPASE
                                                                                                                                                                       PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML--
                                                                                                                                                                                                  ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                      ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention provides the protein and coding sequences of 444 proteins. These were isolated from expressed sequences tags
                                                                                                                                                                                                                                                                                                                                     Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhou P,
Wehrman
                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   7.48;
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T, Drmanac
                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                     Score 89; DB 5;
Pred. No. 2.7;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J,
: RT;
                                                                                                                                                                                                                                                                                                                                        74;
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                      protein of the invention
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                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                      583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren
                                                                                                                                                                                                                                                                                                                                        74;
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                                                                                                                                                                                                                                                                                                                                          Gaps
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422

YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ 478

---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-----

QCAVC---LOPFCHLYWGCTRTGCYGCLA 522

99

153 566

밁 S 밁

523

PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML-

----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA

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The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC complementary strand of a polynucleotide which comprises or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary to a polynucleotide which comprises a 5'-end
CC complementary to a polynucleotide which comprises a 5'-end
CC complementary to a polynucleotide comprises a 3'-end sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 fucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC particularly full-length cDNAs. The primers are also useful for the
CC particularly full-length cDNAs. The primers are also useful for the
CC particularly full-length cDNAs. The primers are also useful for the
CC constant inventor a proper complementary of the proteins encoded by
CC constant inventor and anino acid sequences; and AAH33162 to AAH3322 represent
CC constant inventor.
                                                 Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer sets for synthesizing polynucleotides,
length cDNAs defined in the specification, and
diagnosis of the abnormality of the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein sequence SEQ ID NO:12100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNAs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
                                                                                                                                                          Sequence
                                                                                                                                                                                                            present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; SEQ ID NO 12100; 2537pp + Sequence Listing; English
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                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX RES
                                                                                Similarity
                                                                                                                                                             652
HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa T,
T, Wakamatsu
                                                                          7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wakamatsu A,
                                                       26;
                                                    Score 89; DB
Pred. No. 2.9;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins encoded by the full-length
                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K,
C, Otsuki
                                                          74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particularly the 5602 full-
d for the detection and/or
                                                                                                      Length 652
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto
                                                          74;
                                                          Gaps
        50
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Mon

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OM protein -
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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| CGD2_6/ptodata/1/iaa/5_COMB.pep:*
| CGD2_6/ptodata/1/iaa/6_COMB.pep:*
| CGD2_6/ptodata/1/iaa/H_COMB.pep:*
| CGD2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
| CGD2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
| CGD2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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351
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US-09-949-016-10829

US-09-949-713A-2

US-09-945-713A-2

US-09-902-540-13214

US-10-104-047-2283

US-08-129-456A-36

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US-09-018-576-3

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Sequence 12, Appli
Sequence 12, Appli
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Sequence 19049, A
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Sequence 13214, A
Sequence 13214, A
Sequence 3283, Ap
Sequence 33, Appli
Sequence 3, Appli
Sequence 31, Appli
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ALIGNMENTS

ACID SEQUENCES RELATING TO FOR DIAGNOSTICS AND THERAPEUTICS

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Sequence 6596, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

ITILE OF INVENTION: NUCLEIC ACID AND ANINO AC:

TITILE OF INVENTION: ENTEROCOCCUS FAECALIS FOI

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 6596

LENGTH: 158
                                                                                                          ; ratent No. 5268463
; APPLICANT: JEFFERSON,
TITLE OF INVENTION: P
; CONSTRUCT
                                                                                                                                                                        RESULT 2
5268463-7
;Patent No. !
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Best Local Similarity
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                NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 119,102
                                                                                                                                                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                    191 PLSE----KIAELKEKIVLTHNRLKSLMKIL 217
                                                                                                                                                                                                                                                                                                                                                                                                 134 LLFCGSCGIPVGFHLYSTHAALAAL---ROHFCLSSDKWVCYLLKTKAIVNASEMDIQNV 190
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                                                                                                                                                                                                                                                                             PISKTVTRKLSDLSYK-DLYYQEMK-LLKII 157
                                                                                                                                       JEFFERSON, RICHARD
NVENTION: PLAANT PRO
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26.5%;
                                                            US/07/447,976
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Pred. No. 0.18;
7; Mismatches
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RESULT 3
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NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 15-OCT-1993
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Patent No. 5879906
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Best Local
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                                                                                                           GENERAL INFORMATION:
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APPLICATION NUMBER: 447,976
FILING DATE: 08-DEC-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
APPLICATION NUMBER: 119,102
APPLICANT: Jefferson, Richard A.
APPLICANT: Wilson, Katherine J.
APPLICANT: Leader, Michael
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JEFFERSON, RICHARD A.
TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E.COLI
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APPLICATION NUMBER: 264,
FILING DATE: 31-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 WSLPVALVALAIASIGQGVTMTVMWALEADTVEYGEYLTGVR--IEGLTYSLFSFTRKCG
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37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                WDLSRSLGAVVFSRVTNNV-----VLEA-----PFLVGIEGSLKGSTYNLL-FCGSCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIAELKEKIVLTHNRLKSLMKILSEVT 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 81.5; D ilarity 25.2%; Pred. No. 2.9; Conservative 30; Mismatches
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25.2%; Pred. No.
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US-09-151-957-6
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Matches
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Patent No. 6429292
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/882,704A
FILING DATE: 25-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5879906tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98104-772
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: PSTEM: $1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/882,704A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
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STRANDEDNESS: sir
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,957
FILING DATE: 11-Sep-198
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GLUCURONIDE REPRESSORS NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jefferson, Richard A.
Wilson, Katherine J.
Leader, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 QAIG---GSIPAFILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTD 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 WSLPVALVALAIASIGQGVTMTVMWALEADTVEYGEYLTGVR--IEGLTYSLFSFTRKCG 374
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                                                                                                                                                                                                                               STATE: Washington
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                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                              ADDRESSEE: SEED and BERRY LLP
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6300 Columbia Center,
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PRIOR APPLICATION DATA:

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Patent No.
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                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,930
FILLNG DATE: 21-NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
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INFORMATION FOR SEQ ID NO:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OLMSTED, ELIZABETH A.
APPLICANT: MAURO, LAURA J.
APPLICANT: DAVIS, ALAN R.
APPLICANT: DIXON, JACK E.
TITLE OF INVENTION: OSTEOBLAST-TITLE OF INVENTION: PHOSPHATASE
                                                         REGISTRATION NUMBER: 34,202
REFERENCE/FOCKET NUMBER: 20344-20975.00
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
           TELEFAX: 706141
                      TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: No. 6429292tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 QAIG---GSIPAFILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTD 431
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 29.6%;
Matches 21; Conservative
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                                                                                                                                                                  Matches
                                                                                                                                                                                 Best Local
                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                TELEFAX: 732/594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1711 amino ac
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gerhold, David L.
TITLE OF INVENTION: CYCLIN-DEPENDENT PROTEIN KINASE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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ZIP: 07065-0907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, RY60-30
                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                 LENGTH:
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120 LVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSD----
                                  102 AQVKSYLQMLLKGV---AFCHA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 DLSRSLGAVVF 106
                                                              64 PQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVV----LEAPF 119
                                                                                                  43 GFPNQALREIKALQEME-DNQYVVQLKAVFPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQ 101
                                                                                                                               22 GGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLG----

    1: 1711 amino acids
amino acid

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732/594-4720
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                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                  6.6%; Score 78.5; I
23.2%; Pred. No. 3.8;
ative 24; Mismatches
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Pred. No. 28;
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                                     ----NNIVHRDLKPANL 133
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US-09-018-576-12
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 732/594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1988
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
TELEPAX: 732/594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATOR - DOS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gerhold, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 LISASGQLKIADFGLARVFS---PDGSRLY-THQ--VATRSVGCIMGELLNGSPLFPGKN 187
                                                                                                                              120
225
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 S 225
                                                          --KMVCYLLKTKAIVNASEM-DIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQ 224
                                                                                                                                                                                            PQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVV----LEAPF
                               DIEQLCYVLRILGTPNPQVWPELTELPDYNKIS-FKEQVPMP------
                                                                                              LISASGQLKIADFGLARVFS---PDGSRLY-THQ--VATRSVGCIMGELLNGSPLFPGKN
                                                                                                                            LVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSD------
                                                                                                                                                            AQVKSYLQMLLKGV---AFCHA-----
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P.O. Box 2000, RY60-30
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23.2%; Pred. No. 3.8;
Ltive 24; Mismatches
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CYCLIN-DEPENDENT PROTEIN KINASE
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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ZIP: 07065-0907
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                                                                                            168 -- KMVCYLLKTKAIVNASEM-DIONVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQ 224
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237 S
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                                                                                                                                                                                                                                                                                                                          1 Similarity 23.2 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 325 amino acids amino acid
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P.O. Box 2000, RY60-30
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23.2%;
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CYCLIN-DEPENDENT PROTEIN KINASE
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Pred. No. 3
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RESULT 10

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Sequence 237, Application US/09771161A Patent No. 6936450 GENERAL INFORMATION: APPLICANT: LEVINE, et al.
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Best Local Similarity
Matches 56; Conserv
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APPLICANT: Gerhol
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: lines
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ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, RY60-30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 07065-0907
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23.2%; Pred. No. 3.8;
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PILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR PPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
SEQ ID NO 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-19049
Sequence 19049, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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LENGTH: 190
TYPE: PRT
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                    QPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAG
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    RPCRHTRRCVRPAAGGYPG---RAGDRAS----
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milarity 32.9%;
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                                                                            Score 78; DB 2
Pred. No. 1.9;
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Pred. No. 6
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    ----VARSTGPGLPAAPGRPRGHC- 139
                                                                                                                Length 190;
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64 POLPSWLOPERCA 76

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APPLICANT: KOIDE, YOSHINAO

APPLICANT: NAKANISHI, YUJi

APPLICANT: SUZUKI, SACOTU

ITITLE OF INVENTION: LALPHA-GLYCEROPHOSPHATE OXIDASE GENE, REC

TITLE OF INVENTION: L-ALPHA-GLYCEROPHOSPHATE OXIDASE GENE

FILE REPERENCE: A20-121814C/KI

CURRENT APPLICATION NUMBER: US/09/537,682

CURRENT FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1
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; TYPE: PRT
; ORGANISM: Enterococcus faecium No. 6303357 7044
US-09-537-682-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08520933 Patent No. 5981194
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Jeffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TAKEUCHI, Kenichi
APPLICANT: KOIDE, Yoshinao
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                      APPLICANT: Yamada, Tatsuo
APPLICANT: Kennard, Malcolm
TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                           STREET: 40 King
CITY: Toronto
STATE: Ontario
                                                                COUNTRY: Cana
ZIP: M5H 3Y2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 LLPIYEDEGATTFNMF------SVKVAMDLYDKLANVTGTKYENYTLTPEEVLEREPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 DFAEGT-----SSRSTKLVHGGIRYLKTFDVEVV--ADTVGERAVVQGIAPHIPKPDPM 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 DFCGGTERAIDQASFTTSM-----EWDTQVVKGSSPLGP----AGLGAEEPAAGPQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGDQÍVGVKARDL----LTDEVIEIKSKLVI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTKAIVNASEMDIQNVPLSEKIAELKEKIVL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LK--KEGLKGA------GVYLDFRNNDARLVIDNIKKAAEDGAYLVSKMKAVGFLY 202
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                                                                                                                                                 40 King Street West
                                                                                       Canada
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Rothenberger, Sylvia
Food, Michael R.
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Best Local S
Matches 59
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Patent No. 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     APPLICANT: Food, Michael R. APPLICANT: Yamada, Tatsuo APPLICANT: Yamada, Malcolm TITLE OF INVENTION: Use of p9' TITLE OF INVENTION: as Diagno NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Shona S. McDiarmid REGISTRATION NUMBER: 38,798 REFERENCE/DOCKET NUMBER: 761 TELECOMMUNICATION INFORMATION: TELEPHONE: 416-364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,933
FILING DATE: August 31, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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nes 59; Conserv
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                                                                                                            COUNTRY:
                                                                                                                                                       CITY: Toronto
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                                                                                              RY: Canada
M5H 3Y2
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PatentIn Release #1.0, Version #1.25
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King Street West
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as Diagnostic and Therapeutic
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19;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,040
FILING DATE: 01-APR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRAVELLe, Micheline
REGISTRATION UMBER: 40,261
REFERENCE/DOCKET NUMBER: 7685-032
TELECOMMUNICATION INFORMATION:
TELEPHAN: 416-361-1398
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CLARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acids
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Search completed: November 18, 2005, 20:35:56
Job time : 50 secs
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                                                                                                376 IQCVSAKSP 384
                                                                                                                                                                                           333 MKGLLC-DPNRLPPYLRWCVLSTPEIQKCGDM-----
                                                                                                                                                                                                                                           158 LRGHFCLSSDKMVCYL----LKTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSL 213
                                                                                                                                                                                                                                                                                           277 LN----EGQRLFSHEGSSFQMFSSEAYGQKDLLFKDSTSELVPIATQTYEAWLGHEYLHA 332
                                                                                                                                                                                                                                                                                                                              110 TNNVVLEAPFLYGIEGS----LKGSTY---NLLFCGSCG--IPVGFHLYST---HAALAA 157
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protein -9

protein search, using

Title: Perfect score:

US-09-942-052A-728 1198

Sequence 59, Appl Sequence 158084, Sequence 968, App Sequence 968, App Sequence 57058, A Sequence 44924, A Sequence 44919, A

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51058, A 51058, A 38, Appl 59, Appl 59, Appl

Sequence

Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match

100%

Database

6.5.4.2.2.1

Searched:

Scoring table:

BLOSUM62 Gapop 10.0 ,

Sequence 66220, A Sequence 6, Appli Sequence 31748, A Sequence 115342, Sequence 1618, Ap Sequence 281194,

66220, A 6, Appli 31748, A 115342,

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Total number of hits satisfying chosen parameters:
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Publication No. US20030170626A1

GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Hobert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: OF INVENTION: UNCLBIC ACID AND CORRESPONDING PROTEIN ENTITLE OF INVENTION: UNSETUL IN TREATMENT AND DETECTION OF CANCER
FILLE REFERENCE: 51158-20028.00

CURRENT APPLICATION NUMBER: US/09/942,052

CURRENT APPLICATION NUMBER: US/09/942,052

CURRENT FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: 60/228,432

PRIOR FILING DATE: 2000-08-28

PRIOR FILING DATE: 2000-08-28

VERENT FILING DATE: 2000-08-28

SOFTWARE: PAT INFORM OFFICE OFFI
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Best Local Similarity
Matches 229; Conserv
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US-10-195-518-6
US-10-430-763-31748
US-10-437-963-115342
US-10-631-467-1618
US-10-425-115-281194
US-10-425-115-281194
US-10-425-136-59
US-10-957-135-59
US-10-450-763-44919
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Result No.

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US-09-942-052-729

Sequence 729, Application No. US200 GENERAL INFORMATION:

Application US/09942052 b. US20030170626A1

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TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: U5/09/942,052
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 729
     APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Challita-Bid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/90/942,052
CURRENT APPLICATION NUMBER: 06/228,432
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 730
LENGTH: 229
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OTHER INFORMATION: protein sequence
-09-942-052-729
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APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                  APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
TYPE: PRT
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Best Local Similarity
Matches 229; Conserv
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APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
CURRENT FILING DATE: 2001-08-28
CURRENT FILING DATE: 2001-08-28
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PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
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o. US20030170626A1
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Pred. No. 9.8e-114;
; Mismatches 0;
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; NAME/KEY: MOD RES
; LOCATION: (93)
; OTHER INFORMATION: Unknown amino acid or stop
US-09-942-052-707
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SOTTWARE: PatentIn Ver. 2.1
SEQ ID NO 707
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Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILLING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
             APPLICANT: Ge, WANGMAO
APPLICANT: Challia-Eid, Pia M.
APPLICANT: Challia-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
CURRENT FILING DATE: 2001-08-28
                                                                                                                                                                APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
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LOCATION: (50)..(51)
OTHER INFORMATION: Unknown amino acid
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TYPE: PRT
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OTHER INFORMATION: Unknown
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NT FILING DATE: 2001-08-28
APPLICATION NUMBER: 60/228,432
                                                                                                                                                                                                                                                                                                                                                                                                                               162 FCLSSDKMVCYLLKTKAIVNASEMDIQNVPLSEKIAELK 200
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Challita-Eid,
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Afar, Daniel
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Pred. No. 1.2e-05;
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APPLICANT: Seishi KATO
APPLICANT: Chikashi EGUCHI
APPLICANT: Chikashi EGUCHI
APPLICANT: Chikashi EGUCHI
TITLE OF INVENTION: Human Proteins and cDNAs thereof
FILE REFERENCE: 2001-1102A/WMC/00653
CURRENT APPLICATION NUMBER: US/09/890,688
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: JP 11-346863
PRIOR APPLICATION NUMBER: JP 11-34684
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
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US-09-890-688-82
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SEQ ID NO 704
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Best Local !
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2000-31062 PRIOR FILING DATE: 2000-02-08 PRIOR APPLICATION NUMBER: JP 2000-34091
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ORGANISM: Unknown Organism
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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APPLICATION NUMBER: JP 2000-34090
FILING DATE: 2000-02-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-02-14
APPLICATION NUMBER: JP 2000-35899
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                                      150 STHAALAALRGHFCLSSDKMVCYLL--KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTH 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                             91 VHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
                                                                                                                                                                        49 ASMWSSMSEDASV----ADMERAQL--EEBAAAAB-----ERPLVFLCSGCRRPLGDS
                                                                                                                                                                                                                 31 ASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS
                                                                                                                                                                                                                                                                                   Similarity
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CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 209
                                                                               --LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGYVYR 153
                                                                                                                                                                                                                                                            Conservative
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Pred. No. 0.0075;
0; Mismatches 88
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208 NRIKSIMKILSE

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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 969
LENGTH: 233
TYPE: DET
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; Sequence 195427, Application US/10437963
; Publication No. US20040123343A1
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 195427 LENGTH: 708
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 969, Application US/10408765A Publication No. US20040101874A1
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Best Local &
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 9.4%; Score 113; DB 4; Length 233; Local Similarity 27.1%; Pred. No. 0.0075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 ASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRLKSLMKILSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGYVYR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASMWSSMSEDASV----ADMERAQL--EEEAAAAE-----ERPLVFLCSGCRRPLGDS
                                                                                                                                                                                                          Wu, Wei
Boukharov, Andrey
Barbazuk, Brad
                                                                                                                                                                                             Li, Ping
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; TYPE: PRT; ORGANISM: Oryza sativa; FEATURE: ; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_91377C.1.pep US-10-437-963-195427
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US-10-437-963-154548
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US-10-437-963-154548
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 154548
LENGTH: 361
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Publication No. US20040123343A1
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                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Local Similarity 24.5%;
hes 71; Conservative 3:
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153
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                                    EAPFLVGIEGSLKGSTYNLL--FCGSCGI-----PVGFHLYSTHAALAAL-----RGH
                                                                                                                AGPQLP----SW--LQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou, Yihua
Cao, Yongwei
Wu, Wei
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                                                                                                                                                         APTPLPFRRAVRAKAAQDGSGGTSSASPAVAST-----DVVVVPGSREATPSG-PASDPV 102
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                                                                           AGRGSPAAVLSWEELQVEMGRLLEAGA--RVIGREIAEARGLEHRM-----SELGNN---- 152
----LSEIRGSLR-VTYTGLHQLAGKCGIKSTIPANPDEFSLTSSLAELAAAMEEIPSKH
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                                                                                                                                                                                                                                                       Score 92; DB 4; Length 361; Pred. No. 1.9;
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RESULT 12
US-09-780-525-2
; Sequence 2, Application US/09780525
; Patent No. US20020004223A1
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US-10-369-493-18389
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LENGTH: 695
TYPE: PRT
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Best Local Similarity
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                                                  NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052)B
                                                                                                                   APPLICANT: Xiaotong Li
TITLE OF INVENTION: FHAR1, A NEW RING FINGER PROTEIN
FILE REFERENCE: GP-70668-C1
CURRENT APPLICATION NUMBER: US/09/780,525
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/456,876
PRIOR APPLICATION NUMBER: 09/456,876
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APPLICANT: Yuan Zhu
APPLICANT: Priya Chaturvedi
APPLICANT: Mark R. Hurle
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ORGANISM: HOMO SAPIENS
                                   LENGTH: 664
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US-10-437-963-186569
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 186569
LENGTH: 435
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Matches
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                               Local
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                                                                                                           116 EAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLK 175
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                                    176 TKAIVNASEMDIQN-----VPLSEKIAELKEKIVLTH 207
                                                                           136 EGPF---
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                                                                                                                                                   89 EDPSPOPGVPLILLP-----LCCRCYAKHICSEYVVRTTDLVNHI------LNSNAIS
                                                                                                                                                                                   58 EEPAAGPQLPSWLQPERCAVFQCAQCHA--VLADSVHLAWDLSRSLGAVVFSRVTNNVVL 115
                                                                                                                                                                                                                          41 APEPLSCRHGRHLRCAAVD-----GGAGRETERPSPPAPQ-----REESPSGSLGAAL
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                                                                                                                                                                                                                                                           2 AAQPL--RH--RSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGA 57
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                                                                                                                                                                                                                                                                                                                   h 7.4%; Score 88.5; D
Similarity 22.9%; Pred. No. 5.6;
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 NGSFGGITEDEEQSSLYNFLYPSKELLPDDKEMSIFDH 211
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                                                                           SMRKARFLGSAS---AFSVKQTEWP---
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RESULT 14 US-10-437-963-155606

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RESULT 15
US-10-282-122A-51802
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US-10-437-963-155606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 155606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 155606, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                 Sequence 51802, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                     APPLICANT: Wang,
APPLICANT: Zamud
APPLICANT: Malon
APPLICANT: Hasel
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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APPLICANT:
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                     TITLE OF
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(848)
OTHER INFORMATION: unsure at all Xaa locations
                                     APPLICANT:
                                                          APPLICANT:
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   REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                174 LKTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKP 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 GSKAMECGVKMCLVGWPWLAWDELGPRSGYQFGLNHRRPLVKAVLDGHLCEEEDAVNCLP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAGPQLPSWLQPERCAVFQCAQCH------AVLADSVHLAWDLSR----
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INVENTION: Identification SRENCE: ELITRA.034A
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                                                                Carr, Grant
Carr, Robert
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Barbazuk, Brad
                                     ŭ,
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Wall, Daniel
                                                                                                                                                                                                       Zamudio, Carlos
Malone, Cheryl
                                                                                                                                                                    Ohlsen, Kari
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                                                    Forsyth, R.
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                     of Essential Genes
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                     'n
                     Microorganisms
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; LENGTH: 669
TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51802
Search completed: November 18,
Job time : 168 secs
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PRIOR FILLING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILLING DATE: 2001-02-09
PRIOR FILLING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%; Score 86.5; D
Best Local Similarity 27.4%; Pred. No. 16;
Matches 37; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 51802
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
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PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/230,347 PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                366 DIGRKKVKIGSRVFVRRSNDVI---PEIMGVTEETEGETNEIEAPTICPYCGSEIVKEGV
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                                                                                                                                                                                                                423
                                                                                                                                                                                                                                                         147 HLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIVNASEMDIQNVP-LSEKIAB-LKEKIV 204
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                                                                                                        LNIKSISDLYRITKE
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Minimum DB
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and is derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US05 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/US1 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US1 NEW PUB.pep:*
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 GenCore version 5.1.6
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US-11-022-562-235
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US-10-036-263A-8
US-10-036-263A-8
US-10-131-826A-212
US-10-467-962B-95
US-10-467-962B-95
US-10-131-826A-302
US-11-074-176-82
US-10-131-826A-302
US-10-97-831-2
US-10-97-831-2
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US-10-97-831-2
US-10-131-826A-418
US-10-131-826A-418
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Sequence 235, App
Sequence 3, Appli
Sequence 13, Appli
Sequence 4, Appli
Sequence 172, App
Sequence 172, App
Sequence 101, App
Sequence 212, App
Sequence 212, App
Sequence 212, App
Sequence 30, Appl
Sequence 20, Appl
Sequence 272, App
Sequence 272, App
Sequence 272, App
Sequence 272, App
Sequence 302, Appl
Sequence 304, Appli
Sequence 4, Appli
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ALIGNMENTS	US-10-939-890-501	US-10-939-890-500	US-10-967-457-18	US-10-131-826A-108	US-10-689-742-170	US-11-082-389-208	US-10-816-768-63	US-10-816-768-62	US-10-816-768-52	US-11-074-176-54	US-11-074-176-314	US-10-131-826A-480	US-11-082-389-86	US-10-652-893-4	US-11-082-389-220	US-10-627-633-6	US-10-627-633-2	US-10-131-826A-308	US-10-816-768-49	US-11-012-762-26
	Sequence 501, App	Sequence 500, App	Þ		Sequence 170, App	•	70	Sequence 62, Appl	•	•	•	•	ъ		Sequence 220, App	Sequence 6, Appli	Sequence 2, Appli	Sequence 308, App	Sequence 49, Appl	Sequence 26, Appl

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; SEQ ID NO 235
, LENGTH: 1255
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-235
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US-11-022-562-235
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Best Local (
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652 IGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAI
                     144 VGFHLYSTHAALAALRG------HFCLSSDKMVCYLLKTKAI 179
                                               608 TAIHADQLTPAWR------IYSTGNNVPQTQAGCLIGAEH--VDTSY-----ECDIP
                                                                         84 HAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIP 143
                                                                                                                           29 DQASFTTSM-EWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQC----
                                                                                                                                                    Ch 5.7%; Score 68; DB 1 Similarity 21.8%; Pred. No. 8; 36; Conservative 24; Mismatdhes
                                                                                                                                                                                DB 7; Length 1255
                                                                                                                                                           69; Indels
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                                                                                                                                                           Gaps
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Sequence 3, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: Sasaki, Ken

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US-11-013-759-13
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; TYPE: PRT
; ORGANISM: MOTAXELLA CATATHALIS
US-11-013-759-13
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Publication No.
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                                                                                                                                                                                                                                                                                                             SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
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PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Sasaki, Ken
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TYPE: PRT
ORGANISM: Moraxella catarrhalis
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                                                                          GKSTLNDGGLSIKNPTGSEQI --
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FAKVNNNGVVGA----GIDGTTRITRDEIGFTGTNG-----
                                    FSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLS
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Klein, Michel
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                                                                                                                                                       Conservative
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22.0%; Pred. No. 18;
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22.0%; Pred. No. 18;
tive 20; Mismatches
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Sequence 7, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
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APPLICANT: LOOSMOZE, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR PRIOR DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.1
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LENGTH: 2047
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                                                                                        TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE TITLE OF INVENTION: PROTEIN OF MORAXELLA FILE REFERENCE: 1038-921MIS:jb CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
                   PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                      APPLICANT: LOOSMORE, Sheena APPLICANT: Sasaki, Ken APPLICANT: Yang, Yan Ping APPLICANT: Klein, Michel H.
SOFTWARE: PatentIn Ver.
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Local Similarity 22.0%; Pred. No. 18;
Les 40; Conservative 20; Mismatches
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; TYPE: PRT
; ORGANISM: Moraxella
US-11-013-759-7
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US-10-336-263A-8
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Best Local S
Matches 23
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Matches
Sequence 8, Application US/10336263A Publication No. US20050251882A1 GENERAL INFORMATION:
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SEQ ID NO 172
LENGTH: 381
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Best Local Similarity
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PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 231
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APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766,000091.10
CURRENT APPLICATION NUMBER: US/10/689,742
CURRENT FILING DATE: 2003-10-22
CURRENT FILING DATE: 2003-10-22
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                      126 SLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVC 171
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Evans, Cheryl
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LaVallie, Edward
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22.0%; Pred. No. 18;
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21.7%; Pred. No. 1.8;
ative 19; Mismatches 42; Indels
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RESULT 8
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PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 101
LENGTH: 680
TYPE: PRT
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TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTE
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: 38-21 (52176) A
CURRENT APPLICATION NUMBER: US/10/336,263A
CURRENT FILING DATE: 2003-01-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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Publication No. US20050246784A1
GENERAL INFORMATION:
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APPLICANT: Klein, Mathieu
TITLE OF INVENTION: Identification of Herbicidally Active Substances
FILE REFERENCE: 2000 857
CURRENT APPLICATION NUMBER: US/10/467,962B
CURRENT FILLING DATE: 2003-08-14
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ORGANISM: Nostoc punctiforme
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE LOCATION: (1)..(48 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 480
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 5.5%; Score 66; DB 1; Length 480; Local Similarity 28.9%; Pred. No. 3.3; es 22; Conservative 14; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 YSTHAALAALRGHF-CLSSDKWYCYLLKTKAIVNASEMDIQNVPLSEKIAELKEKIVLTH 207
                                                                         534 GRFNDAIECLEEMKSVGLKPSSTMYNALINAYAQRGLSEQAVNAFRVMTSDGLKPSLLAL
                                                                                                                                                                 477
594 NSLINAFGEDRRDABAFAVLQYMKENGVKPDVVTYT---TLMKALIRVDKFQKVP 645
                                    177 KAIVNASEMDIQNVPLSEKIAELKEK----IVLTHNRLKSLMKILSEVTPDQSKP 227
                                                                                                                  130 STYN-----LLFCGSCGIPVGFHLYSTHAALAALRG-----HFCLSSDKMVCYLLKT 176
                                                                                                                                                                                                      73 ERCAVFQCAQCHAVLADSV--HLAW-DLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKG
                                                                                                                                                                                                                                               43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSTQGVAARVHELYQSLTLDTFIQEIIKTKKLTPDLERQIQNL------LKSK-VLKS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIKALEKLIDSFSND 473
                                                                                                                                                               ERRGCLPCATTYNIMINSYGDQERWDDMKRLLGKMKSQGILPNVVTHTT-LVDVYG--KS
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Duff, Stephen M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blau, Astrid
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                             5.4%; Score 65; DB 24.6%; Pred. No. 7; rative 25; Mismatches
                                                                                                                                                                                                                                                                                      DB 1; Length 680
                                                                                                                                                                                                                                                    81;
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RESULT

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US-10-467-962B-95
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                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Homo Sapien
US-10-131-826A-212
Sequence 95, Application US/10467962B Publication No. US20050246784A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 212, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 212
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
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Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 74
TYPE: PRT
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APPLICATION NUMBER: 60/059113
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059115
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APPLICATION NUMBER: 60/059117
FILING DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/059352 FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/059263 FILING DATE: 1997-09-18
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                                                                                                                                                560 AAPELAMGALELESRNSTLDPGKPEMMKSPTNTTPHVPAEGPEASRP 606
                                                                                                                                                                                                                               509 CSACHNERLDVPV----WDVEATLNFLKAHFSPSN-----IILDFPAAGSAARRDVONVA 559
                                                                                                                                                                                    192 LSEKIA----ELKEKIVLTHNRLKSLMKILSEVT-----PDQSKP 227
                                                                                                                                                                                                                                                                      137 CGSC----GIPVGFHLYSTHAALAALRGHFCLSSDKWVCYLLKTKAIVNASEMDIQNVP 191
                                                                                                                                                                                                                                                                                                            th 5.2%; Score 62.5; I Similarity 24.3%; Pred. No. 15; 26; Conservative 18; Mismatches
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Gurney, Austin L.
Sherwood, Steven
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Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumas, Daniel
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CURRENT APPLICATION NUMBER: US/10/467,962B

CURRENT FILING DATE: 2003-08-14

PRIOR APPLICATION NUMBER: PCT/EP02/01466

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PATENTIN VETS. 2.0

SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/997,201A
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 60/524,840
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/10997201A Publication No. US20050249739A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marasco, Wayne
APPLICANT: Sui, Jianhua
TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
FILE REFERENCE: 20363-026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Plesch, Gunnar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 592
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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nes 32; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAA-----
                                      144 VGFHLYSTHAALAALR 159
                                                                              604 TAIHADQLTPAWR-----IYSTGNNVFQTQAGCLIGAEH--VDTSY-----ECDIP 647
                                                                                                                                                            550 DVSDFTDSVRDPKTSEILDISPCAFGGVSVITPGTN-----ASSEVAVLYODVNCTDVS 603
                                                                                                               84 HAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIP 143
                                                                                                                                                                                                29 DQASFTTSM-EWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQC----
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IGAGICASYHTVSLLR 663
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                               Score 60.5;
Pred. No. 21;
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US-11-074-176-80
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US-11-074-176-222
                                                              US-11-074-176-222
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Matches
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SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 80
LENGTH: 614
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                                                                                                                                      NUMBER OF SEQ ID NOS: 381
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 222
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 222, Application US/11074176 Publication No. US20050250135A1 GENERAL INFORMATION:
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Best Local Similarity
Query Match
Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Ust
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/551,161 PRIOR FILING DATE: 2004-03-08
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                                                                                                                                                                                                                                                                                                   APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Us
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Klaenhammer, Todd R. APPLICANT: Russell, William M. APPLICANT: Altermann, Eric APPLICANT: MCAuliffe, Olivia
                                                                                                                                                                                                                                                                                    FILE REFERENCE: 5051-694
                                                                       TYPE: PRT ORGANISM: Lactobacillus acidophilus
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                                                                                                                   LENGTH: 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 DNALKDAGLTVN-DIDKVILNGGSTRIPAVQKAVKEWAGKEPDHSINPDEAVALGAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 ERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNGIVNVSAKDM-GTGKEQKIT-IKSSSGLSDEEIKRMQKDAEEHAEEDKK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSKSQIFSTAADNQPAVDVHVLQGERPMAADDKTLGRFELTDIPPAPRGVPQIQVTFDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVLADSVHLAWDLSRSLGAVVFSRVTNNVVLE-APFLVGIEGSLKGSTYNLLFCGSCGIP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altermann, Eric
McAuliffe, Olivia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/11074176
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  4.9%;
22.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60;
Pred. No.
  Score 58.5;
Pred. No. 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 100;
    33;
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                       DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 614
                                                                                                                                                                                                                                                                                                         Uses Therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uses
                    Length
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US-10-512-184-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3; OTHER INFORMATION: specificity against Fusarium ssp.; originates; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27
                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                             US-10-131-826A-302
                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                           Sequence 302, Application US/10131826A Publication No. US20050245730A1
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V. TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant TITLE OF INVENTION: antibody fragments and fusions mediated plant disease TITLE OF INVENTION: resistance against fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2004-10-22 NUMBER OF SEQ ID NOS: 72
                                   APPLICANT:
                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 GAVVFS---RVTNNV-----VLEAP---FLVGIEGSLKGSTYNLLFCGSCGIFVGFHL
                                                                                                                                                                                                                                                                                                                                          156 GGTVK-ITCSGSTAHYSWHQQKSPGSAPVTLISFNNQRPSDIPSRFSGSKSGSTGTLTIT
                                                                                                                                                                                                                                                                      215 GVRAEDEAVYYCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
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                                                                                                                                                                                                                                                                                                      69 WLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAP 118
                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HNRLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYLVFSLANTITNGVLFYLYKFVIGKPGEFWVVGLIATIIG-----FCVSPMFPI-LNK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERAI--DQASFTTSMEWD------TQVVKGSSPLGPAGLGAEEPAAGPQLPSW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIPRKWL-FIAGQTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAFAAVISALAIICAIIVCFGTKEKHNLIRNSAKQKTTLRQVFSAIFHNDQILWP---SL
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                                                                                                                         Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                            GGTERAIDQASFTTSMEWDTQVVKGSSPL-----GPAGL-----GAEEPAAGPQLPS 68
                Gao, Wei-Qiang
Gerritsen, Mary E.
                                                  Desnoyers, Luc
Filvaroff, Ellen
Goddard, Audrey
                                                                                        DeForge, Laura
                                                                                                       Beresini, Maureen
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                                                                                                                                                                                                                                                                                                                                                                                                                                  4.8%; Score 58;
24.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MICAYLLFIFCRONVVLMDLGLILFNINFAQLVTVLTLTD 369
                                                                                                                                                                                                                                                                      ----GWD--RSITAGLFGAGTTLTVLGQP
                                                                                                                                                                                                                                                                                                                                                                                                                   Migmatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71;
                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HLAWDLSRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 302
LENGTH: 421
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-302

4.8%: Score 58; DB 1; Length 421;
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT FAPPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
Search completed: November 18, 2005, 20:49:50 Job time : 8 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                  141 GIPVGFHLYSTHAALAALRGHFCLSS--DKWVCYLLKTKAIVNASEMDIQNVPLSEKIAE 198
                                                                                                                         105 AVTANSFINATHLKE-INLSHNKIKS 129
                                                                                                                                                            199 ------LKEKIVLTHNRLKS 212
                                                                                                                                                                                                                                      52 GVP--FHQYT----LGCVSECFCPTNFPSSMYCDNRKLKTIPNI-PMHIQQLYLQFNEIE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Timothy A.
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Regult.
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Maximum DB
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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B540788
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RESULT 2 D71293 D71293 D71293 D71293 C; Describer: Treponema pallidum subsp. pallidum (syphilis spirochete) C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 C; Accession: D71293 R; Fraser, C.M.: Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi. rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDr. rson, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998 A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Reference number: A71250; MUID:98332770; PMID:9665876 A; Accession: D7123 A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA		Query Match 7.7%; Score 92; DB 2; Length 695; Best Local Similarity 25.3%; Pred. No. 2; Matches 38; Conservative 28; Mismatches 50; Indels 34; Gaps 7; Matches 38; Conservative 28; Mismatches 50; Indels 34; Gaps 7; Qy 101 LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG 160	A; Accession: C86731 A; Status: preliminary A; Cross-references: UNIPROT:Q9CH87; UNIPARC:UPI00000C6919; GB:AE005176; PID:g12723778; FA; Experimental source: strain IL1403 C; Genetics: C; Genetics: A; Grene: copb A; Grene: copb A; Grene: copb C; Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding (RESULT 1 C86731 C86731 C95per-potassium transporting ATPase B copB [imported] - Lactococcus lactis subsp. lact: copper-potassium transporting ATPase B copB [imported] - Lactococcus lactis subsp. lact: c;Species: Lactococcus lactis subsp. lactis c;Species: Lactococcus lactis subsp. lactis c;pate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C;Accession: C86731 C;Accession: C86731 R;Bolottin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrll R;Bolottin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrll A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subspaces number. As625; MIID:11317471

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A; Experimental :
C; Genetics:
A; Gene: TP0695
A43623

Kanamycin kinase (EC 2.7.1.95) - Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 31-Dec-2004
C;Accession: A43623
C;Ferover, F.C.; Gilbert, T.; O'Hara, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DKFZp434N2420.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change C;Accession: T46399 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.;
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A;Accession: T46399
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52; Conserv
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                                                                                                                                                                                                                                                        PMPDRRAEREQDPRVAPQ
                                                                                                                                                                  ALAALRGHFCLS-----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                                                                                                                PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML--
                                                                                                                                                                                                                           ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                    ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-----
                                                                                                                                                                                                                                                                                                                 YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ
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Se: strain Nichols
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Plasmid 22, 52-58, 1989
A,Title: Nucleotide sequence of a novel kanamycin resistance
A,Feference number: A43623; MUID:89387451; PMID:2550983
A,Accession: A43623
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: Tope: Japan
Glutamate synthase (NADH2) (EC 1.4.1.14) precursor [validated] - G:Species: Medicago sativa (alfalfa) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C:Accession: JQ1977; PQ0551 R:Gregerson, R.G.; Miller, S.S.; Twary, S.N.; Gantt, J.S.; Vance Plant Cell 5, 215-226, 1993 A;Title: Molecular characterization of NADH-dependent glutamate A;Reference number: JQ1977; MUID:93200806; PMID:8453303 A;Accession: JQ1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the A.Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAD-dependent DNA ligase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change C;Accession: A97229
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C;Superfamily: 1
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A;Cross-references: UNIPROT:Q97FQ5; UNIPARC:UPI00000CA5D7;
A;Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                       205 LTHNRLKSLMKILSE 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
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33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               HLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIVNASEMDIQNVP-LSEKIAE-LKEKIV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIGRKKVKIGSRVFVRRSNDVI---PEIMGVTEETEGETNEIEAPTICPYCGSEIVKEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLSR---SLGAVVFSRVTNNVVLBAPFLVGİEGSLKGSTYNL-----LFCGSCGIPVGF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFIDHPIKYI---ECLVNALHQLQAIDIRNCPFSSKIDVRLKELKYLLDNRIADI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSDKMVCYLLKTKAIVNA----SEMDIQNVPLSEKI-AELKEKIVLTHNRLKSL 213
                                                                                                                                                                                                                                                                                                  LNIKSISDLYRITKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Scilarity 27.4%; Pr
Conservative 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                     --FC--ENTLSCKPOMVKSIVHFASREAMNIEGFSEKTAEOLFEK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.5; DI
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 88; DB
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-Sep-2001 #text_change 31-Dec-2004
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                                                                                                                                                                                   [validated] - alfalfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250
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                                                                                                Vance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE001437; PIDN:AAK80620.1;
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                                                  synthase
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                                                                                                C.P.
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                                                       from alfalfa
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C;Comment: This enzyme catalyzes the reductive transfer of the amido group C;Superfamily: glutamate synthase (NADH/NADPH), eukaryotic type C;Keywords: 3Fe-4S; chloroplast; iron-sulfur protein; metalloprotein; NAD; F;1-101/Domain: propeptide #status predicted <PRO>
F;1-101/Domain: propeptide #status predicted <PRO>
F;102-2194/Product: glutamate synthase (NADH) #status experimental <MAT>
F;102-Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 102-114 <GR2>
A; Cross-references: UNIPARC: UPI0000172061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-2194 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2074
C;Accession: AE2074
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, M.; Yasuda, M.; Tabata,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferrichrome binding protein of ABC transporter all2147 [imported] - Nostoc
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A; Residues: 1-361 < KUR>
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;1246,1252,1257/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily:
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                                                                                                                                                 145 GFHLYSTHAALAALRGHFCLSSDKWVCYLLKTKAIVNASEMDIQNVPLSBKIAELKEKIV
  164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%;
Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANPA---ARISVKLVSEAGVGVIASGVVKGHAEHVLISGHDGGTGASRWTGIKSAGLPWE
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                                               LTHNRLKSLMKILSEVTP 222
                                                                                                                                                                                                                                                      LSRSLGAVVF----SRVT---NNVVLEAPFLVGIEGSLKGSTYNLLFCGSC-----GIPV 144
  LGLTWLKSSYKILSSIAP 181
                                                                                                                                                                                                      ISHALGKVKIPLKPQRVVVLEENIILDSVLALGVK-----PVGVMYCQDCEENFRGIP-
                                                                                                                                                                                                                                                                                                                                                                                                       ferrichrome-iron transport protein
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                                                                                                                                                                                                                                                                                                        17; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                  Score 84.5;
Pred. No. 4.
                                                                                                       LLADVPVVG----NIGNOPSLEKILSLKPDLI
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterials (Before and Comparative Analysis)
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              formate hydrogenlyase, iron-sulfur subunit 2 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: B69099
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A; Residues: 1-663 < KUR>
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A;Experimental source: strain Delta H
C;Genetics:
                                                                                                                                                                                                                                                                      A;Gene: MTH1736
C;Superfamily: nrfC protein; ferredoxin 2[4Fe-4S] homology
F;62-118/Domain: ferredoxin 2[4Fe-4S] homology <FER2>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-143 < MTH>
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Best Local
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les 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNL-----LFCGSCGIPVGFHLYSTHAAL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468
126 SLKGSTYNLLFCGSC--GIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIVNAS
                                                                                                                       72 PERCAVFOCAOCHAVLADSVHLAWDLSRSLGAVVF-----SRVTNNVVLEAPFLVGIEG
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                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKILSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRITKE
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                                                                            PELCD--ECMKCERICPKNAIRVID-----GVPVFCMHCSPERAPCINICPEDAIVEVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                   6.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                             Score 82.5; DI
Pred. No. 2.1;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                               DB 2; Length 143;
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                                                                                                                                                                                  66;
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                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE001437; PIDN:AAK79167.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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C;Species: Arabidopsis thallana (mouse-ear cress, C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: A85433 R;anonymous, The European Union Arabidopsis Genome Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
A85433
                                                                                                                                                                                                                             R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sugar transporter like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-493 <STO>
A;Cross-references: UNIPROT:023213; UNIPARC:UPI000009F22F; GB:NC_001268; NID:g7270615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-493 <S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A85001; A; Accession: A85433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
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                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-967 < STO>
                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 20-A;
C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                               A;Cross-references: UNIPROT:Q9A2U2; UNIPARC:UPI00000C7AB1; GB:AE005673; NID:g13425184;
                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       NA polymerase I [imported] - Caulobacter crescentus;Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
                                                                                 Superfamily:
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                                                                                                                           Genetics:
Matches
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position: 4
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                                                                                                        CC3464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 QCAQCHAVLADSVHLAWDLSRSLGAVVF---SRVTNNVVLEAPFLVGI-----EGSLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
Similarity 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                        F87678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALAALRG-----HFCLSSDKWVCYLLK---TKAIVNAS---EMDIQNVP---LSEKIA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRTSDIIGRRYTIVLASILFMLGSILMGWGPNYPVLLSGRCTAGLGVGFALMVAPVYSAE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVVILEDRCIGCGLCRDACPVG--AITLNERGVAVKCDLCIDRDKPLCVMVCPKGALSES 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELKE--KIVLTHNRLKSLMKILSEV--TPDQSK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IATASHRGLLASLPHLCISIGILLGYIVNYFFSKLPMHIGWRLMLGIAAVPSLVLAFGIL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMPESPRWLIMOGRIKEGKEILELVSNSPEEAE
                                                                                 DNA-directed DNA polymerase
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%;
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                   6.8%; Score 82;
24.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
  27;
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Pred. No. 1
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    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                          DB 2; Length 967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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72;
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  Indels
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62;
  Gaps
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    11;
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  R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; D. Nature 409, 529-533, 2001
                                                                                                     A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H85767 A;Status: preliminary
                                                                                 A; Molecule type:
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Date: 16-Feb-2001 #sequence_revision 16-Feb-2001; Accession: H85767

u, B.; Glasr Dimalanta,

Glasner, lanta, E.;

Potamousis, J.D.; Rose,

D.J.; Mayhew
K.; Apodaca,

#text_change

09-Jul-2004

Escherichia coli

(strain O157:H7, substrain

DNA

GB:AE005174; NID:g12515601;

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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

8;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transport protein, probable [imported] C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision
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D90404
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RESULT 13
H85767
glucuronide permease [imported] -
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-329 < KUR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A99139
A; Accession: D90404
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                                                                                                                                                                                                                                                                                                                                                                 Best
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                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 MVCYLLKTKAIVNASEMDIQNVPLSEKIAELK 200 : : | : : | : : | : | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 VTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 APVVSVSYMGAAARAAHPVEPVKIDHAAYACVRDLATLKAWVAKATD----KGLVAFDT
                                                                                                                                                       167
                                                                                                                                                                                           93
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                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATPPRGDFCGGTERAIDQ---ASFTTSMEWDT---QVVKGSSPLGPAGLGAEEPAAGPQ
                                                                                                                                                                                             VRFLVGVIFGLLTSYAVESAVKSGRNVLVGFTTAGWPIGWVI--
                                                                                                                                                                                                                                 APFLVG----
                                                                                                                                                                                                                                                                    LSESMHLAYWEVFAIVALPFLGRIIGSFIYQVFKNSVISYCFPFLGFLVILQNFLGALIF 92
                                                                                                                                                                                                                                                                                                          LADSVHLA-WD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ISHCEKADGLAFEAPADIEQIPLADVIATLK 443
                                                                                                                                                      DKMVCY-LLKTKAIVNASEMDIQNVPLSE---KIAELKEKIVLTHNRLKSLMKILSEVTP 222
                                                                                                                  -SYVAYVLLKUWNVINISGILIMLLALFELNGKEFGERSKISVSFPRLTSILIYVSALTP
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable [imported]
                                                                                                                                                                                                                                                                                                                                                                 6.8%;
22.2%;
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                                                                                                                                                                                                                               IEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QPERC--AVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSR 108
                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                          -LSRSLGAVVFSRVTNNVV---
                                                                                                                                                                                                                                                                                                                                                                 Score 81.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                 Mismatches
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucuronide permease [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: C90919
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                                                                               C;Accession: B6491B
C;Accession: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64918
                                                                                                                                                                                                                glucuronide permease uidB - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: B64918
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C;Superfamily: melibiose carrier protein
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90919
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                               A;Status: nucleic
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                                                               acid sequence not shown; translation not
                                                                                                                                                                     Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
UNIPROT: P30868; UNIPARC: UPI0000137B23; GB: AE000257; GB: U00096; NID:
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A;Experimental source: strain K-12, substrain MG1655 C;Genetics;
A;Gene: uidB; gusB
A;Gene: uidB; gusB
C;Superfamily: melibiose carrier protein
C;Superfamily: melibiose carrier protein
C;Keywords: carrier protein; transmembrane protein
C;Keywords: transmembrane #status predicted <TM01>
F;37-53/Domain: transmembrane #status predicted <TM02>
F;152-168/Domain: transmembrane #status predicted <TM03>
F;154-200/Domain: transmembrane #status predicted <TM05>
F;231-247/Domain: transmembrane #status predicted <TM06>
F;310-326/Domain: transmembrane #status predicted <TM07>
F;310-326/Domain: transmembrane #status predicted <TM07>
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Copyright (c) 1993 - 2005 Compugen Ltd.
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A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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B EMBL, AKO14084; BAB2J47.1; -; mRNA.
B RISHMIJSG00000022978; Mus musculus.
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MEDLINB=20530913; PubMed=11078861; DOI=10.1101/gr.152600;

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Bukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=237631;
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                                                                 preliminary data.
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                            "Functional annotation of a Nature 409:685-690(2001).
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S (TrEMBLrel. 30,
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                                                                             full-length mouse cDNA collection.";
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Yoghino M., Itoh M., Fukuda
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Balda E., Dragani T.A., Plettcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Garimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Garimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Wanny Y., Watanabe Y., Wells C.,
RA Wilning L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilning L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
                                                                                                  CSTRAIN-15-7BL/6J; TISSUE=Whole body;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiracka T., Hori F.,

A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Kawai J., Kojima Y., Owa C., Saito H., Nomura K., Numazaki R., Ohno M.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Muramatsu M., Hayashizaki Y.;

A Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CSTBL/63; TISSUE=Whole body;
MEDILNE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDILNE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa Y., Isawa M., Ohara E.,
Yoneda Y., Ishikawa T., Ozawa Y., Isawa M., Ohara E.,
Yoneda Y., Ishikawa T., Ozawa Y., Isawa M., Ohara E.,
Yoneda Y., Ishikawa T., Ozawa Y., Isawa M., Ohara E.,
Yoneda Y., Ishikawa T., Ozawa Y., Isawa M., Ohara E.,
Yoneda Y., Ishikawa T., Ozawa Y., Isawa M., Ohara E.,
Yoneda Y., Ishikawa T., Ishikawa T., Ishikawa M., Ishikawa T., Ishikawa M., Ishikawa M., Ishikawa M., Ishikawa T., Ishikawa M., Ishikawa M., Ishikawa 
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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Nature 420:563-573(2002).
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
NUCLEOTIDE SEQUENCE
STRAIN=C57BL/6; TIS
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Cassavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wullahy S.J.,

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A Bosak S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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16-OCT-2001
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Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AK012533; BAB28302.1; -; mRNA.
EMBL; BC079990; AAH79900.1; -; mRNA.
Ensembl; ENSMUSG0000022978; Mus musculus.
MGI; MGI:1913828; 2610039C10Rik.
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MEDLINE=20237674; PubMed=10773462; DOI=10.1016/S0378-1119(00)00089-5; Slavov D., Hattori M., Sakaki Y., Rosenthal A., Shimizu N., Minoshima S., Kudoh J., Yaspo M.-L., Ramser J., Reinhardt R.,
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                                                                                                     NUCLEOTIDE SEQUENCE.
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c. Natl. Acad. Sci. U.S.A.
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A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences,"

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Wakamatsu A., Kimura K., Sakamoto K., Hatano N
Saito K., Kojima S., Sugiyama T., Ono T., Okano
Aotsuka S., Sasaki N., Hattori A., Okumura K.,
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC PubMed=15164055; DOI=10.1038/nature02564; Watanabe H., Fujiyama A., Hattori M., Tay. Kuroki Y., Noguchi H., Benkahia
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STRAIN-Singapore local strain; TISSUE=Embryo;

KK MEDIINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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Kang J., Hong L., Schaefer T.E.,

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Stapleton M., Gudin T.B., Toshiyuki S., Carninci P., Prange C.,

Kana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Bloecker H., Hellmann I., Khaitovich P., Paabo S., Reinhardt R.,
Elneng H.-J., Zhang X.-L., Zhu G.-F., Wang B.-F., Fu G., Ren S.-X.,
Zhao G.-P., Chen Z., Lee Y.-S., Cheong J.-E., Choi S.-H., Wu K.-M.,
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
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Name=LOC553502;
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SEQUENCE 232 AA; 25832 MW;
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Last annotation update)
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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                                                                                                                                RA Suggang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q., RA Bankier A.T., Lehmann R., Hamlin N., Davise R., Gaudet P., Fey P., RA Bankier A.T., Lehmann R., Hamlin N., Davise R., Gaudet P., Fey P., RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Ra Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C., RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., RA Kerhornou T., Haydock S., van Driessche N., Cronin A., Goodhead I., RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., RA Kerhornou T., Haydock S., van Driessche N., Cronin A., Goodhead I., RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C., RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C., RA Hauser H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M. Grushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M. A., Spiegler S., Tivey A., RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y., Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C., RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., R., Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., R., Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R., R., Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., Cox E.C., Phathyl, Cannon and C., Chutton. The sequence shown here is derived from an C. Chutton. The sequence shown here is derived from an C. Chutton.
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NIH MGC Project;
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Schnerch A., Schein
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Schein J.E., Jones S.J.!
and initial analysis of r
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Dictyosteliida; Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                      Tanaka Y.,
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Rutherford K.M., Rutter S., Squares S., McDonald S.,
RA Rutherford K.M., Rutter S., Squares R., Squares S.,
RA Rutherford K.M., Rutter S., Squares R., Squares S.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Waitehead S.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehare V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RT MILLETYN. To, human C210rf45
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10-MAY-2005 (Rel. 47, Last annotation update)
Hypothetical protein C970.12 in chromosome III.
ORFNames=SPCC970.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9P802;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
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                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724; Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
GeneDB
                  EMBL; AL031530;
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Schizosaccharomycetales; Schi:
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                                                                                       the Swiss Institute of Bioinfo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNVPLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCIYSLFYCSYCNSPLGRKYNKTSQKFKILNNHFVVDIGSITYYSVGGNNNIIVEDKNEI
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                CAB72327.1; -;
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22.9%;
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Pred. No. 0.
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RESULT 11
Q4Q626_LEIMA
ID Q4Q626;
AC Q4Q626;
DT 13-SEP-2005 (TrEMBLrel. 31,
DT 13-SEP-2005 (TrEMBLrel. 31)
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Best Local &
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SEQUENCE
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                                                                                                                                                                                                                                                Hypothetical SEQUENCE 15
                                                                                                                                                                                                                                                                        Peacock C.S., Murphy L., Ivens A.C., Bérriman M., Blackwell J., Smith D., Collins M., Fosker N., Harrin D., Oliver K., O'Neil S., Saunders D., Seger K., Warren T., Rajandream M., and Barrell B.G.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL, CT005268; CAJ08424.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. ORFNames=LmjF31.2350;
                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                         STRAIN=Friedlin;
                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005515; F:protein binding; IPI.
GO:0031055; P:chromatin remodeling at centromere;
GO:0007059; P:chromosome segregation; IMP.
GO:0016575; P:histome deacetylation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0031066; P:regulation of histone deacetylation plete proteome; Hypothetical protein. UENCE 155 AA; 17874 MW; A7AEBD0F93760B0B CRC64;
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972
                       175 KTKAI
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                                                                                                                        66 LPSWLQPERCAVFQCAQCHAVLADSV-----
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                                                                         FLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVC----YLL
                                                                                                                                                                        GGTERAIDQASFTTSME-----WDTQVVKGS-----SPLGPAGLGAEEPAAGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPERCAVFQCAQCHAVLADSVHLAWDLSRS--LGAVVFSRVTNNVVLEAPFLVGIEGSLK 128
                                                                                               ----ARAAIGE--ODFGFLNDTVAAPSTYSHMLCRVLELIRTARLNLILLDVLLQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QP---SVFQCKKCFQIVGDS--NAWVISHREYLSFTLSDAVENSVRVEDTFKRSDDGL--
RNLAV
                                                                                                                                                  GGGELMQTDAGFSIEVESPIAFLYDDDVHRASQDVGQKRAREEPDGVGGAGEEDAAAG--
                                                                                                                                                                                                                                                   1556 AA;
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 976
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                                                                                                                                                                                                                                                    170195 MW;
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Last sequ
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Pred. No. 0.13;
8; Mismatches 61;
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                                                                                                                                                                                                                           Score 94;
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                                                                                                                                                                                                                                                    F6FF7CDDFE8DCA59 CRC64;
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                                                  SADKASCVIGMWLL
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RESULT 12
Q8S611 ORYSA
ID Q8S611 ORYSA F
AC Q8S611;

PRELIMINARY;

PRT;

361

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update)

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PARSULT PRESULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DO DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESER
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Best Local S
Matches 61
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OSCH87_LACLA PRELIMINARY; PRT; 695 AA.

OSCH87;

OJCH87;

OJCH87;

OJCH87;

OJCH87;

OJCH87;

OJCH87;

OLJUN-2001 (TrEMBLrel. 17, Last sequence update)

OLJUN-2001 (TrEMBLrel. 26, Last annotation update)

OLMAR-2004 (TrEMBLrel. 26, Last annotation update)

Copper-potassium transporting ATPase B.

Name=copB; OrderedLocusNames=LL0851;

Name=copB; OrderedLocusNames=LL0851;

Name=copB; OrderedLocusNames=LL0851;

Name=copB; OrderedLocusNames=LL0851;
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SEQUENCE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-FBB-2005 (TrEMBLrel. 29, Last annotation update)
Putative gypsy-type retrotransposon protein.
ORFNames=OSJNBa0096E22.5;
STRAIN=II1403;
MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
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EMBL; AC099400; AAL91599.1; -; Genomic DNA.
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The Rice Chromosome 10 Sequer
"In-depth view of structure,
chromosome 10.";
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Wing R.A., Yu Y., Soo
Saski C., Henry D., (
Submitted (MAR-2002)
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                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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., Oates R., Simmons J.;
02) to the EMBL/GenBank/DDBJ
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Lactobacillales; Streptococcaceae; L
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Pred. No. 6.4;
28; Mismatches
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6.4;
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II lactis ssp. lactis III403.";
II denome Res. 11:731-733(2001).
IR EMBL, AB006319; AAX04949.1; -; Genomic_DNA.
IR PIR; C86731; C86731.
IR GO; GO:0016021; C:integral to membrane; IEA.
IR GO; GO:0016020; C:membrane; IEA.
IR GO; GO:0005524; F:Arp binding; IEA.
IR GO; GO:0003824; F:catalytic activity; IEA.
IR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid.
IR GO; GO:0016820; F:metal ion binding; IEA.
IR GO; GO:0046872; F:metal ion binding; IEA.
IR GO; GO:000452; P:metal ion transporter activity; IEA.
IR GO; GO:0008152; P:metal ion transport; IEA.
IR GO; GO:0008152; P:metal ion transport; IEA.
IR GO; GO:0015992; P:metal ion transport; IEA.
IR GO; GO:0015992; P:metal ion transport; IEA.
IR GO; GO:0015992; P:metal ion transport; IEA.
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Best Local S
Matches 38
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InterPro; IPR005834; Dehal like !
InterPro; IPR008250; E1-E2 ATPASE
Pfam; PF00122; E1-E2 ATPASE; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATANPASE.
     InterPro;
PROSITE; F
SEQUENCE
                                                                                                                                                      Sasaki T., Matsumoto T.,
"Oryza sativa nipponbare(
clone:P0023E10.";
                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI TaxID=39947;
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TIGREAMS; TIGRO1511; ATPASE-IB1 Cu; 1.
TIGREAMS; TIGRO1525; ATPASE-IB hvy; 1.
TIGREAMS; TIGRO1494; ATPASE_B1_E2; UNKNOWN_1.
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InterPro; IPR006416; ATPase B1-E2.
InterPro; IPR001757; ATPase B1-E2.
InterPro; IPR005834; Dehal_Tike_hyd:
                                                                             Gramene; Q69KE0;
                                                                                                        Submitted (NOV-2002) to the EMEMBL; AP005934; BAD36600.1; -;
                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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38; Conserv
        PS00216; SUGAR TRANS
628 AA; 68281 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMGMNFWFELATLIVIMLIGHLIEMKAIMGAGDALKDLASLVPKKAHLKSGKDVELSELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAELKEKIVLTHNRLKSLMKILSEVTPDQS 225
IPR005829; Sug_transporter.
IPR005829; Sug_transport 1; UNKNOWN 1.
PS00216; SUGAR_TRANSPORT 1; UNKNOWN 1.
628 AA: 68281 MW; 3230B108C6061027 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695
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ilarity 25.3%;
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                                                                                                                                                                                Hattori M., (GA3) genomic
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Last annotation updat
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Pred. No. 1
                                                                                                   EMBL/GenBank/DDBJ
-; Genomic_DNA.
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                                                                                                                                                                                Sakaki Y., Katayo
DNA, chromosome
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mosome 9,
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Best Local
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375; Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R.J., Gwinn M.L., Hickey B.K., Clayton R.A., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.J. Scherger B., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky Pujii C., Garland S.A., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Phosphoribosylglycinamide formyltransferase, putative.
OrderedLocusNames=TP0695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O83693 TREPA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                GO; GO:0016874; F:ligase activity; IEA.
InterPro; IPR003135; ATP-grasp.
InterPro; IPR001761; ATP GRASP.
Pfam; PF02222; ATP-grasp; 1.
PROSITE; PS50975; ATP-GRASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Nichols;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treponema pallidum.
Bactaria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 281:375-388(1998).
EMBL; AE001243; AAC65662.1; -; Genomic_DNA.
PIR; D71293; D71293.
TIGR; TP0695; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Treponema pallidum, spirochete.";
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54 GLGAEEPAAGPQLPSWLQP-ERCAVFQC--AQCHAVLADSVHLAWDLSRSLGAVVFSRVT 110
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                                                                                                                                                                                                                                                                                                        proteome.
597 AA;
                                                                                     CALP--GHRLEATKNATDKTRMRACFTRARLRCPRFTFLEPDSFAWDT-----PPGHA
                                                                                                                                      CATPPRGDFCGGTERAID----QASFT-----TSMEWDTQVVKGSSPLGPA
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28.0%;
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Pred. No.
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Pred. No. 17
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                                                                                                                                                                                                                                               Length 597;
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                            GRVIIE-EFIVGREFSLEG----LIFDGT----
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arch completed: November 18, 2005, 20:35:05 b time : 237 secs

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